

SEQUENCE LISTING FREE TEXT

dgoA CDS for KDPGal Aldolase

dgoA CDS for KDPGal Aldolase

dgoA CDS for KDPGal Aldolase

aroB CDS for DHQ Synthase

tktA CDS for major Transketolase isozyme

tktB CDS for minor Transketolase isozyme

Primer JWF 430

Primer JWF 449

Primer JWF 484

Primer JWF 529

Primer JWF 501

Primer JWF 499

Primer JWF 541

Primer JWF 542

Primer JWF 610

Primer JWF 611

Primer JWF 625

Primer JWF 626

Primer JWF 541

Primer JWF 542

Primer JWF 636

Primer JWF 637

Primer JWF 669

Primer JWF 670

Primer JWF 599

Primer JWF 560

Primer JWF 484

Primer JWF 529

SEQUENCE LISTING

<110> Board of Trustees operating Michigan State University
Frost, John W.

<120> Methods and Materials for the Production of Shikimic Acid

<130> 6550-000086

<150> US 60/505,658

<151> 2003-09-24

<160> 34

<170> PatentIn version 3.3

<210> 1

<211> 618

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(615)

<223> dgoA CDS for KDPGal Aldolase

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ttc gac gcg gtt gaa atc ccg ctg aat tcc cca caa tgg gag caa agc	144
Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Gln Ser	
35 40 45	
att ccc gcc atc gtt gat gcg tac ggc gac aag gcg ttg att ggc gca	192
Ile Pro Ala Ile Val Asp Ala Tyr Gly Asp Lys Ala Leu Ile Gly Ala	
50 55 60	
ggt acg gta ctg aaa cct gaa cag gtc gat gcg ctc gcc agg atg ggc	240
Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly	
65 70 75 80	
tgt cag ctc atc gtt acg ccc aat atc cat agt gaa gtg atc cgc cgt	288
Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg	
85 90 95	
gcg gtg ggc tac ggc atg acc gtc tgc ccc ggc tgc gcg acg gcg acc	336
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100 105 110	

gaa gcc ttt acc gcg ctc gaa gcg ggc gcg cag gcg ctg aaa ata ttt 384
 Glu Ala Phe Thr Ala Leu Glu Ala Gly Ala Gln Ala Leu Lys Ile Phe
 115 120 125
 ccg tca tcg gct ttt ggt ccg caa tac atc aaa gcg tta aaa gcg gta 432
 Pro Ser Ser Ala Phe Gly Pro Gln Tyr Ile Lys Ala Leu Lys Ala Val
 130 135 140
 ttg cca tcg gac atc gca gtc ttt gcc gtt ggc ggc gtg acg cca gaa 480
 Leu Pro Ser Asp Ile Ala Val Phe Ala Val Gly Gly Val Thr Pro Glu
 145 150 155 160
 aac ctg gcg cag tgg ata gac gca ggt tgt gca ggg gcg ggc tta ggc 528
 Asn Leu Ala Gln Trp Ile Asp Ala Gly Cys Ala Gly Ala Gly Leu Gly
 165 170 175
 agc gat ctc tat cgc gcc ggg caa tcc gta gag cgc acc gcg cag cag 576
 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
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 195 200 205

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 <213> Escherichia coli

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35 40 45

Ile Pro Ala Ile Val Asp Ala Tyr Gly Asp Lys Ala Leu Ile Gly Ala
50 55 60

Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly
65 70 75 80

Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg
85 90 95

Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr
100 105 110

Glu Ala Phe Thr Ala Leu Glu Ala Gly Ala Gln Ala Leu Lys Ile Phe
115 120 125

Pro Ser Ser Ala Phe Gly Pro Gln Tyr Ile Lys Ala Leu Lys Ala Val
130 135 140

Leu Pro Ser Asp Ile Ala Val Phe Ala Val Gly Gly Val Thr Pro Glu
145 150 155 160

Asn Leu Ala Gln Trp Ile Asp Ala Gly Cys Ala Gly Ala Gly Leu Gly
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Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
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195 200 205

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<223> dgoA CDS for KDPGal Aldolase

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Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser
35 40 45

att ccg cag gtc gtc gac gct tac ggc gag cag gcg ctt atc ggc gcg 192
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50 55 60

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Gly Thr Val Leu Gln Pro Glu Gln Val Asp Arg Leu Ala Ala Met Gly
 65 70 75 80
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 Cys Arg Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg
 85 90 95
 gcg gtg ggt tac ggc atg acc gtg tgt cca ggc tgc gcc acc gcc agc 336
 Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Ser
 100 105 110
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 Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe
 115 120 125
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 Pro Ser Ser Ala Phe Gly Pro Asp Tyr Ile Lys Ala Leu Lys Ala Val
 130 135 140
 ctg ccg ccc gag gtt ccg gtc ttt gcc gtt ggc ggc gtg acg ccg gaa 480
 Leu Pro Pro Glu Val Pro Val Phe Ala Val Gly Gly Val Thr Pro Glu
 145 150 155 160
 aac ctg gcg cag tgg att aat gcc ggc tgt gtt ggg gca gga ttg ggt 528
 Asn Leu Ala Gln Trp Ile Asn Ala Gly Cys Val Gly Ala Gly Leu Gly
 165 170 175
 agc gat ctc tat cgt gcc ggc cag tcg gtt gaa cgt acc gcg cag cag 576
 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
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 <213> *Klebsiella pneumoniae*

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 35 40 45
 Ile Pro Gln Val Val Asp Ala Tyr Gly Glu Gln Ala Leu Ile Gly Ala
 50 55 60

Gly Thr Val Leu Gln Pro Glu Gln Val Asp Arg Leu Ala Ala Met Gly
65 70 75 80

Cys Arg Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg
85 90 95

Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Ser
100 105 110

Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe
115 120 125

Pro Ser Ser Ala Phe Gly Pro Asp Tyr Ile Lys Ala Leu Lys Ala Val
130 135 140

Leu Pro Pro Glu Val Pro Val Phe Ala Val Gly Gly Val Thr Pro Glu
145 150 155 160

Asn Leu Ala Gln Trp Ile Asn Ala Gly Cys Val Gly Ala Gly Leu Gly
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<222> (1)..(615)
<223> dgoA CDS for KDPGal Aldolase

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Thr Pro Asp Asp Ala Leu Ala His Val Gly Ala Val Val Asp Ala Gly
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ttt gac gct ata gaa att ccg ctt aac tcc cca cag tgg gaa aaa agc 144
 Phe Asp Ala Ile Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser
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 Ile Ser Ser Val Val Lys Ala Tyr Gly Gly Arg Ala Leu Ile Gly Ala
 50 55 60
 ggt acc gta ctg aaa ccg gaa cag gta gac cag ctt gcc ggg atg ggc 240
 Gly Thr Val Leu Lys Pro Glu Gln Val Asp Gln Leu Ala Gly Met Gly
 65 70 75 80
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 Cys Lys Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg
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 gcg gtg agc tat ggc atg acc gtg tgt ccg ggc tgc gcc acg gca acg 336
 Ala Val Ser Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr
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 gaa gcc ttt tct gcg ctg gat gca ggc gca cag gcg tta aaa att ttc 384
 Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe
 115 120 125
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 Pro Ser Ser Ala Phe Gly Pro Gly Tyr Ile Ser Ala Leu Lys Ala Val
 130 135 140
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 Leu Pro Pro Asp Val Pro Leu Phe Ala Val Gly Gly Val Thr Pro Glu
 145 150 155 160
 aac cta gcg caa tgg att aaa gca ggc tgt gtg ggc gcg gga ttg ggt 528
 Asn Leu Ala Gln Trp Ile Lys Ala Gly Cys Val Gly Ala Gly Leu Gly
 165 170 175
 agc gat ctc tat cgc gcc ggg caa tcc gtt gaa cgc acc gcg cag cag 576
 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln
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 35 40 45
 Ile Ser Ser Val Val Lys Ala Tyr Gly Gly Arg Ala Leu Ile Gly Ala
 50 55 60
 Gly Thr Val Leu Lys Pro Glu Gln Val Asp Gln Leu Ala Gly Met Gly
 65 70 75 80
 Cys Lys Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg
 85 90 95
 Ala Val Ser Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr
 100 105 110
 Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe
 115 120 125
 Pro Ser Ser Ala Phe Gly Pro Gly Tyr Ile Ser Ala Leu Lys Ala Val
 130 135 140
 Leu Pro Pro Asp Val Pro Leu Phe Ala Val Gly Gly Val Thr Pro Glu
 145 150 155 160
 Asn Leu Ala Gln Trp Ile Lys Ala Gly Cys Val Gly Ala Gly Leu Gly
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Ile Ala Ser Gly Leu Phe Asn Glu Pro Ala Ser Phe Leu Pro Leu Lys	
20 25 30	
tcg ggc gag cag gtc atg ttg gtc acc aac gaa acc ctg gct cct ctg	144
Ser Gly Glu Gln Val Met Leu Val Thr Asn Glu Thr Leu Ala Pro Leu	
35 40 45	
tat ctc gat aag gtc cgc ggc gta ctt gaa cag gcg ggt gtt aac gtc	192
Tyr Leu Asp Lys Val Arg Gly Val Leu Glu Gln Ala Gly Val Asn Val	
50 55 60	
gat agc gtt atc ctc cct gac ggc gag cag tat aaa agc ctg gct gta	240
Asp Ser Val Ile Leu Pro Asp Gly Glu Gln Tyr Lys Ser Leu Ala Val	
65 70 75 80	
ctc gat acc gtc ttt acg gcg ttg tta caa aaa ccg cat ggt cgc gat	288
Leu Asp Thr Val Phe Thr Ala Leu Leu Gln Lys Pro His Gly Arg Asp	
85 90 95	
act acg ctg gtg gcg ctt ggc ggc ggc gta gtg ggc gat ctg acc ggc	336
Thr Thr Leu Val Ala Leu Gly Gly Gly Val Val Gly Asp Leu Thr Gly	
100 105 110	
ttc gcg gcg gcg agt tat cag cgc ggt gtc cgt ttc att caa gtc ccg	384
Phe Ala Ala Ala Ser Tyr Gln Arg Gly Val Arg Phe Ile Gln Val Pro	
115 120 125	
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Thr Thr Leu Leu Ser Gln Val Asp Ser Ser Val Gly Gly Lys Thr Ala	
130 135 140	
gtc aac cat ccc ctc ggt aaa aac atg att ggc gcg ttc tac caa cct	480
Val Asn His Pro Leu Gly Lys Asn Met Ile Gly Ala Phe Tyr Gln Pro	
145 150 155 160	
gct tca gtg gtg gtg gat ctc gac tgt ctg aaa acg ctt ccc ccg cgt	528
Ala Ser Val Val Val Asp Leu Asp Cys Leu Lys Thr Leu Pro Pro Arg	
165 170 175	
gag tta gcg tcg ggg ctg gca gaa gtc atc aaa tac ggc att att ctt	576
Glu Leu Ala Ser Gly Leu Ala Glu Val Ile Lys Tyr Gly Ile Ile Leu	
180 185 190	
gac ggt gcg ttt ttt aac tgg ctg gaa gag aat ctg gat gcg ttg ttg	624
Asp Gly Ala Phe Phe Asn Trp Leu Glu Glu Asn Leu Asp Ala Leu Leu	
195 200 205	
cgt ctg gac ggt ccg gca atg gcg tac tgt att cgc cgt tgt tgt gaa	672

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 Leu Lys Ala Glu Val Val Ala Ala Asp Glu Arg Glu Thr Gly Leu Arg
 225 230 235 240
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 Ala Leu Leu Asn Leu Gly His Thr Phe Gly His Ala Ile Glu Ala Glu
 245 250 255
 atg ggg tat ggc aat tgg tta cat ggt gaa gcg gtc gct gcg ggt atg 816
 Met Gly Tyr Gly Asn Trp Leu His Gly Glu Ala Val Ala Ala Gly Met
 260 265 270
 gtg atg gcg gcg cgg acg tcg gaa cgt ctc ggg cag ttt agt tct gcc 864
 Val Met Ala Ala Arg Thr Ser Glu Arg Leu Gly Gln Phe Ser Ser Ala
 275 280 285
 gaa acg cag cgt att ata acc ctg ctc aag cgg gct ggg tta ccg gtc 912
 Glu Thr Gln Arg Ile Ile Thr Leu Leu Lys Arg Ala Gly Leu Pro Val
 290 295 300
 aat ggg ccg cgc gaa atg tcc gcg cag gcg tat tta ccg cat atg ctg 960
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 305 310 315 320
 cgt gac aag aaa gtc ctt gcg gga gag atg cgc tta att ctt ccg ttg 1008
 Arg Asp Lys Lys Val Leu Ala Gly Glu Met Arg Leu Ile Leu Pro Leu
 325 330 335
 gca att ggt aag agt gaa gtt cgc agc ggc gtt tcg cac gag ctt gtt 1056
 Ala Ile Gly Lys Ser Glu Val Arg Ser Gly Val Ser His Glu Leu Val
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 35 40 45

Tyr Leu Asp Lys Val Arg Gly Val Leu Glu Gln Ala Gly Val Asn Val
 50 55 60

Asp Ser Val Ile Leu Pro Asp Gly Glu Gln Tyr Lys Ser Leu Ala Val
 65 70 75 80

Leu Asp Thr Val Phe Thr Ala Leu Leu Gln Lys Pro His Gly Arg Asp
 85 90 95

Thr Thr Leu Val Ala Leu Gly Gly Gly Val Val Gly Asp Leu Thr Gly
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 115 120 125

Thr Thr Leu Leu Ser Gln Val Asp Ser Ser Val Gly Gly Lys Thr Ala
 130 135 140

Val Asn His Pro Leu Gly Lys Asn Met Ile Gly Ala Phe Tyr Gln Pro
 145 150 155 160

Ala Ser Val Val Val Asp Leu Asp Cys Leu Lys Thr Leu Pro Pro Arg
 165 170 175

Glu Leu Ala Ser Gly Leu Ala Glu Val Ile Lys Tyr Gly Ile Ile Leu
 180 185 190

Asp Gly Ala Phe Phe Asn Trp Leu Glu Glu Asn Leu Asp Ala Leu Leu
 195 200 205

Arg Leu Asp Gly Pro Ala Met Ala Tyr Cys Ile Arg Arg Cys Cys Glu
 210 215 220

Leu Lys Ala Glu Val Val Ala Ala Asp Glu Arg Glu Thr Gly Leu Arg
 225 230 235 240

Ala Leu Leu Asn Leu Gly His Thr Phe Gly His Ala Ile Glu Ala Glu
 245 250 255

Met Gly Tyr Gly Asn Trp Leu His Gly Glu Ala Val Ala Ala Gly Met
 260 265 270

Val Met Ala Ala Arg Thr Ser Glu Arg Leu Gly Gln Phe Ser Ser Ala
275 280 285

Glu Thr Gln Arg Ile Ile Thr Leu Leu Lys Arg Ala Gly Leu Pro Val
290 295 300

Asn Gly Pro Arg Glu Met Ser Ala Gln Ala Tyr Leu Pro His Met Leu
305 310 315 320

Arg Asp Lys Lys Val Leu Ala Gly Glu Met Arg Leu Ile Leu Pro Leu
325 330 335

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<222> (1)..(1989)

<223> tktA CDS for major Tranketolase isozyme

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20 25 30

atg gct gac att gcc gaa gtc ctg tgg cgt gat ttc ctg aaa cac aac 144
Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn
35 40 45

ccg cag aat ccg tcc tgg gct gac cgt gac cgc ttc gtg ctg tcc aac 192
Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn
50 55 60

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Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
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Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys	
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act ccg ggt cac ccg gaa gtg ggt tac acc gct ggt gtg gaa acc acc	336
Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr	
100 105 110	
acc ggt ccg ctg ggt cag ggt att gcc aac gca gtc ggt atg gcg att	384
Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile	
115 120 125	
gca gaa aaa acg ctg gcg gcg cag ttt aac cgt ccg ggc cac gac att	432
Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile	
130 135 140	
gtc gac cac tac acc tac gcc ttc atg ggc gac ggc tgc atg atg gaa	480
Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu	
145 150 155 160	
ggc atc tcc cac gaa gtt tgc tct ctg gcg ggt acg ctg aag ctg ggt	528
Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly	
165 170 175	
aaa ctg att gca ttc tac gat gac aac ggt att tct atc gat ggt cac	576
Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His	
180 185 190	
gtt gaa ggc tgg ttc acc gac gac acc gca atg cgt ttc gaa gct tac	624
Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr	
195 200 205	
ggc tgg cac gtt att cgc gac atc gac ggt cat gac gcg gca tct atc	672
Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile	
210 215 220	
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Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu	
225 230 235 240	
ctg atg tgc aaa acc atc atc ggt ttc ggt tcc ccg aac aaa gcc ggt	768
Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly	
245 250 255	
acc cac gac tcc cac ggt gcg ccg ctg ggc gac gct gaa att gcc ctg	816
Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu	
260 265 270	
acc cgc gaa caa ctg ggc tgg aaa tat gcg ccg ttc gaa atc ccg tct	864
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275 280 285	
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Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu	
290 295 300	
tcc gca tgg aac gag aaa ttc gct gct tac gcg aaa gct tat ccg cag	960

Ser	Ala	Trp	Asn	Glu	Lys	Phe	Ala	Ala	Tyr	Ala	Lys	Ala	Tyr	Pro	Gln		
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Phe	Asp	Ala	Lys	Ala	Lys	Glu	Phe	Ile	Ala	Lys	Leu	Gln	Ala	Asn	Pro		
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ggg	ccg	ctg	ttg	ccg	gaa	ttc	ctc	ggc	ggg	tct	gct	gac	ctg	gcg	ccg		1152
Gly	Pro	Leu	Leu	Pro	Glu	Phe	Leu	Gly	Gly	Ser	Ala	Asp	Leu	Ala	Pro		
	370					375					380						
tct	aac	ctg	acc	ctg	tgg	tct	ggg	tct	aaa	gca	atc	aac	gaa	gat	gct		1200
Ser	Asn	Leu	Thr	Leu	Trp	Ser	Gly	Ser	Lys	Ala	Ile	Asn	Glu	Asp	Ala		
385					390					395					400		
gcg	ggg	aac	tac	atc	cac	tac	ggg	gtt	cgc	gag	ttc	ggg	atg	acc	gcg		1248
Ala	Gly	Asn	Tyr	Ile	His	Tyr	Gly	Val	Arg	Glu	Phe	Gly	Met	Thr	Ala		
			405					410					415				
att	gct	aac	ggg	atc	tcc	ctg	cac	ggg	ggc	ttc	ctg	ccg	tac	acc	tcc		1296
Ile	Ala	Asn	Gly	Ile	Ser	Leu	His	Gly	Gly	Phe	Leu	Pro	Tyr	Thr	Ser		
			420					425					430				
acc	ttc	ctg	atg	ttc	gtg	gaa	tac	gca	cgt	aac	gcc	gta	cgt	atg	gct		1344
Thr	Phe	Leu	Met	Phe	Val	Glu	Tyr	Ala	Arg	Asn	Ala	Val	Arg	Met	Ala		
		435				440					445						
gcg	ctg	atg	aaa	cag	cgt	cag	gtg	atg	gtt	tac	acc	cac	gac	tcc	atc		1392
Ala	Leu	Met	Lys	Gln	Arg	Gln	Val	Met	Val	Tyr	Thr	His	Asp	Ser	Ile		
	450					455					460						
ggg	ctg	ggc	gaa	gac	ggg	ccg	act	cac	cag	ccg	gtt	gag	cag	gtc	gct		1440
Gly	Leu	Gly	Glu	Asp	Gly	Pro	Thr	His	Gln	Pro	Val	Glu	Gln	Val	Ala		
465					470				475					480			
tct	ctg	cgc	gta	acc	ccg	aac	atg	tct	aca	tgg	cgt	ccg	tgt	gac	cag		1488
Ser	Leu	Arg	Val	Thr	Pro	Asn	Met	Ser	Thr	Trp	Arg	Pro	Cys	Asp	Gln		
			485					490					495				
gtt	gaa	tcc	gcg	gtc	gcg	tgg	aaa	tac	ggg	gtt	gag	cgt	cag	gac	ggc		1536
Val	Glu	Ser	Ala	Val	Ala	Trp	Lys	Tyr	Gly	Val	Glu	Arg	Gln	Asp	Gly		
			500					505					510				
ccg	acc	gca	ctg	atc	ctc	tcc	cgt	cag	aac	ctg	gcg	cag	cag	gaa	cga		1584
Pro	Thr	Ala	Leu	Ile	Leu	Ser	Arg	Gln	Asn	Leu	Ala	Gln	Gln	Glu	Arg		
		515					520					525					
act	gaa	gag	caa	ctg	gca	aac	atc	gcg	cgc	ggg	ggg	tat	gtg	ctg	aaa		1632
Thr	Glu	Glu	Gln	Leu	Ala	Asn	Ile	Ala	Arg	Gly	Gly	Tyr	Val	Leu	Lys		

530	535	540	
gac tgc gcc ggt cag ccg gaa ctg att ttc atc gct acc ggt tca gaa Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu 545 550 555 560			1680
gtt gaa ctg gct gtt gct gcc tac gaa aaa ctg act gcc gaa ggc gtg Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val 565 570 575			1728
aaa gcg cgc gtg gtg tcc atg tcg tct acc gac gca ttt gac aag cag Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln 580 585 590			1776
gat gct gct tac cgt gaa tcc gta ctg ccg aaa gcg gtt act gca cgc Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg 595 600 605			1824
gtt gct gta gaa gcg ggt att gct gac tac tgg tac aag tat gtt ggc Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly 610 615 620			1872
ctg aac ggt gct atc gtc ggt atg acc acc ttc ggt gaa tct gct ccg Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro 625 630 635 640			1920
gca gag ctg ctg ttt gaa gag ttc ggc ttc act gtt gat aac gtt gtt Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val 645 650 655			1968
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Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn 35 40 45			
Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn 50 55 60			

Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr
65 70 75 80

Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys
85 90 95

Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr
100 105 110

Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile
115 120 125

Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile
130 135 140

Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu
145 150 155 160

Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly
165 170 175

Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His
180 185 190

Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr
195 200 205

Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile
210 215 220

Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu
225 230 235 240

Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly
245 250 255

Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu
260 265 270

Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser
275 280 285

Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu
 290 295 300
 Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln
 305 310 315 320
 Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp
 325 330 335
 Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro
 340 345 350
 Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe
 355 360 365
 Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro
 370 375 380
 Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala
 385 390 395 400
 Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala
 405 410 415
 Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser
 420 425 430
 Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala
 435 440 445
 Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile
 450 455 460
 Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala
 465 470 475 480
 Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln
 485 490 495
 Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly
 500 505 510
 Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg

515 520 525
 Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys
 530 535 540
 Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu
 545 550 555 560
 Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val
 565 570 575
 Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln
 580 585 590
 Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg
 595 600 605
 Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly
 610 615 620
 Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro
 625 630 635 640
 Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val
 645 650 655
 Ala Lys Ala Lys Glu Leu Leu
 660

<210> 11
 <211> 2004
 <212> DNA
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<220>
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 <223> tktB CDS for minor Transketolase isozyme

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 Met Ser Arg Lys Asp Leu Ala Asn Ala Ile Arg Ala Leu Ser Met Asp
 1 5 10 15
 gcg gta caa aaa gcc aac tct ggt cat ccc ggc gcg ccg atg ggc atg 96
 Ala Val Gln Lys Ala Asn Ser Gly His Pro Gly Ala Pro Met Gly Met

20	25	30	
gct gat att gcc gaa gtg ctg tgg aac gat ttt ctt aaa cat aac cct Ala Asp Ile Ala Glu Val Leu Trp Asn Asp Phe Leu Lys His Asn Pro 35 40 45			144
acc gac cca acc tgg tat gat cgc gac cgc ttt att ctt tcc aac ggt Thr Asp Pro Thr Trp Tyr Asp Arg Asp Arg Phe Ile Leu Ser Asn Gly 50 55 60			192
cac gcg tcg atg ctg ctc tac agt ttg cta cat ctg acc ggt tac gac His Ala Ser Met Leu Leu Tyr Ser Leu Leu His Leu Thr Gly Tyr Asp 65 70 75 80			240
ctg ccg ctg gaa gaa ctg aag aac ttc cgt cag ttg cat tcg aaa acc Leu Pro Leu Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys Thr 85 90 95			288
cca ggc cac ccg gag att ggc tat acg cca ggc gtt gaa acc acc acc Pro Gly His Pro Glu Ile Gly Tyr Thr Pro Gly Val Glu Thr Thr Thr 100 105 110			336
ggc ccg ctt gga caa ggt ttg gcg aac gcc gtc ggg ctg gcg ata gca Gly Pro Leu Gly Gln Gly Leu Ala Asn Ala Val Gly Leu Ala Ile Ala 115 120 125			384
gag cgt aca ctg gcg gcg cag ttt aac cag cca gac cat gag atc gtc Glu Arg Thr Leu Ala Ala Gln Phe Asn Gln Pro Asp His Glu Ile Val 130 135 140			432
gat cac ttc acc tat gtg ttt atg ggc gac ggc tgc ctg atg gaa ggt Asp His Phe Thr Tyr Val Phe Met Gly Asp Gly Cys Leu Met Glu Gly 145 150 155 160			480
att tcc cac gaa gtc tgt tcg ctg gca ggc acg ctg gga ctg ggc aag Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Gly Leu Gly Lys 165 170 175			528
ctg att ggt ttt tac gat cac aac ggt att tcc atc gac ggt gaa aca Leu Ile Gly Phe Tyr Asp His Asn Gly Ile Ser Ile Asp Gly Glu Thr 180 185 190			576
gaa ggc tgg ttt acc gac gat acg gca aaa cgt ttt gaa gcc tat cac Glu Gly Trp Phe Thr Asp Asp Thr Ala Lys Arg Phe Glu Ala Tyr His 195 200 205			624
tgg cat gtg atc cat gaa atc gac ggt cac gat ccg cag gcg gtg aag Trp His Val Ile His Glu Ile Asp Gly His Asp Pro Gln Ala Val Lys 210 215 220			672
gaa gcg atc ctt gaa gcg caa agc gtg aaa gat aag ccg tcg ctg att Glu Ala Ile Leu Glu Ala Gln Ser Val Lys Asp Lys Pro Ser Leu Ile 225 230 235 240			720
atc tgc cgt acg gtg att ggc ttt ggt tcg ccg aat aaa gca ggt aag Ile Cys Arg Thr Val Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly Lys 245 250 255			768

gaa gag gcg cac ggc gca cca ctg ggg gaa gaa gaa gtg gcg ctg gca Glu Glu Ala His Gly Ala Pro Leu Gly Glu Glu Glu Val Ala Leu Ala 260 265 270	816
cgg caa aaa ctg ggc tgg cac cat ccg cca ttt gag atc cct aaa gag Arg Gln Lys Leu Gly Trp His His Pro Pro Phe Glu Ile Pro Lys Glu 275 280 285	864
att tat cac gcc tgg gat gcc cgt gaa aaa ggc gaa aaa gcg cag cag Ile Tyr His Ala Trp Asp Ala Arg Glu Lys Gly Glu Lys Ala Gln Gln 290 295 300	912
agc tgg aat gag aag ttt gcc gcc tat aaa aag gct cat ccg caa ctg Ser Trp Asn Glu Lys Phe Ala Ala Tyr Lys Lys Ala His Pro Gln Leu 305 310 315 320	960
gca gaa gag ttt acc cga cgg atg agc ggt ggt tta ccg aag gac tgg Ala Glu Glu Phe Thr Arg Arg Met Ser Gly Gly Leu Pro Lys Asp Trp 325 330 335	1008
gag aaa acg act cag aaa tat atc aat gag tta cag gca aat ccg gcg Glu Lys Thr Thr Gln Lys Tyr Ile Asn Glu Leu Gln Ala Asn Pro Ala 340 345 350	1056
aaa atc gct acc cgt aag gct tcg caa aat acg ctt aac gct tac ggg Lys Ile Ala Thr Arg Lys Ala Ser Gln Asn Thr Leu Asn Ala Tyr Gly 355 360 365	1104
ccg atg ctg cct gag ttg ctc ggc ggt tcg gcg gat ctg gct ccc agc Pro Met Leu Pro Glu Leu Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser 370 375 380	1152
aac ctg acc atc tgg aaa ggt tct gtt tcg ctg aag gaa gat cca gcg Asn Leu Thr Ile Trp Lys Gly Ser Val Ser Leu Lys Glu Asp Pro Ala 385 390 395 400	1200
ggc aac tac att cac tac ggg gtg cgt gaa ttt ggc atg acc gct atc Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala Ile 405 410 415	1248
gcc aac ggc atc gcg cac cac ggc ggc ttt gtg ccg tat acc gcg acg Ala Asn Gly Ile Ala His His Gly Gly Phe Val Pro Tyr Thr Ala Thr 420 425 430	1296
ttc ctg atg ttt gtt gaa tac gcc cgt aac gcc gcg cgg atg gcg gca Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Ala Arg Met Ala Ala 435 440 445	1344
ctg atg aaa gcg cgg cag att atg gtt tat acc cac gac tca att ggc Leu Met Lys Ala Arg Gln Ile Met Val Tyr Thr His Asp Ser Ile Gly 450 455 460	1392
ctg ggc gaa gat ggt ccg acg cac cag gct gtt gag caa ctg gcc agc Leu Gly Glu Asp Gly Pro Thr His Gln Ala Val Glu Gln Leu Ala Ser 465 470 475 480	1440

ctg cgc tta acg cca aat ttc agc acc tgg cga ccg tgc gat cag gtg	1488
Leu Arg Leu Thr Pro Asn Phe Ser Thr Trp Arg Pro Cys Asp Gln Val	
485 490 495	
gaa gcg gcg gtg ggc tgg aag ctg gcg gtt gag cgc cac aac gga ccg	1536
Glu Ala Ala Val Gly Trp Lys Leu Ala Val Glu Arg His Asn Gly Pro	
500 505 510	
acg gca ctg atc ctc tca agg cag aat ctg gcc cag gtg gaa cgt acg	1584
Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Val Glu Arg Thr	
515 520 525	
ccg gat cag gtt aaa gag att gct cgt ggc ggt tat gtg ctg aaa gac	1632
Pro Asp Gln Val Lys Glu Ile Ala Arg Gly Gly Tyr Val Leu Lys Asp	
530 535 540	
agc ggc ggt aag cca gat att att ctg att gcc acc ggt tca gag atg	1680
Ser Gly Gly Lys Pro Asp Ile Ile Leu Ile Ala Thr Gly Ser Glu Met	
545 550 555 560	
gaa att acc ctg caa gcg gca gag aaa tta gca gga gaa ggt cgc aat	1728
Glu Ile Thr Leu Gln Ala Ala Glu Lys Leu Ala Gly Glu Gly Arg Asn	
565 570 575	
gta cgc gta gtt tcc ctg ccc tcg acc gat att ttc gac gcc cag gat	1776
Val Arg Val Val Ser Leu Pro Ser Thr Asp Ile Phe Asp Ala Gln Asp	
580 585 590	
gag gaa tat cgg gag tcg gtg ttg cct tct aac gtt gcg gct cgc gtg	1824
Glu Glu Tyr Arg Glu Ser Val Leu Pro Ser Asn Val Ala Ala Arg Val	
595 600 605	
gcg gtg gaa gca ggt att gcc gat tac tgg tac aag tat gtt ggt ctg	1872
Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly Leu	
610 615 620	
aaa ggg gca att gtc ggg atg acg ggt tac ggg gaa tct gct ccg gcg	1920
Lys Gly Ala Ile Val Gly Met Thr Gly Tyr Gly Glu Ser Ala Pro Ala	
625 630 635 640	
gat aag ctg ttc ccg ttc ttt ggc ttt acc gcc gag aat att gtg gca	1968
Asp Lys Leu Phe Pro Phe Phe Gly Phe Thr Ala Glu Asn Ile Val Ala	
645 650 655	
aaa gcg cat aag gtg ctg gga gtg aaa ggt gcc tga	2004
Lys Ala His Lys Val Leu Gly Val Lys Gly Ala	
660 665	

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 <212> PRT
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<400> 12

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Ala Asp Ile Ala Glu Val Leu Trp Asn Asp Phe Leu Lys His Asn Pro	35	40	45
Thr Asp Pro Thr Trp Tyr Asp Arg Asp Arg Phe Ile Leu Ser Asn Gly	50	55	60
His Ala Ser Met Leu Leu Tyr Ser Leu Leu His Leu Thr Gly Tyr Asp	65	70	75
Leu Pro Leu Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys Thr	85	90	95
Pro Gly His Pro Glu Ile Gly Tyr Thr Pro Gly Val Glu Thr Thr Thr	100	105	110
Gly Pro Leu Gly Gln Gly Leu Ala Asn Ala Val Gly Leu Ala Ile Ala	115	120	125
Glu Arg Thr Leu Ala Ala Gln Phe Asn Gln Pro Asp His Glu Ile Val	130	135	140
Asp His Phe Thr Tyr Val Phe Met Gly Asp Gly Cys Leu Met Glu Gly	145	150	155
Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Gly Leu Gly Lys	165	170	175
Leu Ile Gly Phe Tyr Asp His Asn Gly Ile Ser Ile Asp Gly Glu Thr	180	185	190
Glu Gly Trp Phe Thr Asp Asp Thr Ala Lys Arg Phe Glu Ala Tyr His	195	200	205
Trp His Val Ile His Glu Ile Asp Gly His Asp Pro Gln Ala Val Lys	210	215	220
Glu Ala Ile Leu Glu Ala Gln Ser Val Lys Asp Lys Pro Ser Leu Ile			

225		230		235		240
Ile Cys Arg Thr Val	Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly Lys					
	245		250		255	
Glu Glu Ala His Gly Ala Pro Leu Gly Glu Glu Glu Val Ala Leu Ala						
	260		265		270	
Arg Gln Lys Leu Gly Trp His His Pro Pro Phe Glu Ile Pro Lys Glu						
	275		280		285	
Ile Tyr His Ala Trp Asp Ala Arg Glu Lys Gly Glu Lys Ala Gln Gln						
	290		295		300	
Ser Trp Asn Glu Lys Phe Ala Ala Tyr Lys Lys Ala His Pro Gln Leu						
	305		310		315	320
Ala Glu Glu Phe Thr Arg Arg Met Ser Gly Gly Leu Pro Lys Asp Trp						
	325		330		335	
Glu Lys Thr Thr Gln Lys Tyr Ile Asn Glu Leu Gln Ala Asn Pro Ala						
	340		345		350	
Lys Ile Ala Thr Arg Lys Ala Ser Gln Asn Thr Leu Asn Ala Tyr Gly						
	355		360		365	
Pro Met Leu Pro Glu Leu Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser						
	370		375		380	
Asn Leu Thr Ile Trp Lys Gly Ser Val Ser Leu Lys Glu Asp Pro Ala						
	385		390		395	400
Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala Ile						
	405		410		415	
Ala Asn Gly Ile Ala His His Gly Gly Phe Val Pro Tyr Thr Ala Thr						
	420		425		430	
Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Ala Arg Met Ala Ala						
	435		440		445	
Leu Met Lys Ala Arg Gln Ile Met Val Tyr Thr His Asp Ser Ile Gly						
	450		455		460	

Leu Gly Glu Asp Gly Pro Thr His Gln Ala Val Glu Gln Leu Ala Ser
 465 470 475 480

Leu Arg Leu Thr Pro Asn Phe Ser Thr Trp Arg Pro Cys Asp Gln Val
 485 490 495

Glu Ala Ala Val Gly Trp Lys Leu Ala Val Glu Arg His Asn Gly Pro
 500 505 510

Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Val Glu Arg Thr
 515 520 525

Pro Asp Gln Val Lys Glu Ile Ala Arg Gly Gly Tyr Val Leu Lys Asp
 530 535 540

Ser Gly Gly Lys Pro Asp Ile Ile Leu Ile Ala Thr Gly Ser Glu Met
 545 550 555 560

Glu Ile Thr Leu Gln Ala Ala Glu Lys Leu Ala Gly Glu Gly Arg Asn
 565 570 575

Val Arg Val Val Ser Leu Pro Ser Thr Asp Ile Phe Asp Ala Gln Asp
 580 585 590

Glu Glu Tyr Arg Glu Ser Val Leu Pro Ser Asn Val Ala Ala Arg Val
 595 600 605

Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly Leu
 610 615 620

Lys Gly Ala Ile Val Gly Met Thr Gly Tyr Gly Glu Ser Ala Pro Ala
 625 630 635 640

Asp Lys Leu Phe Pro Phe Phe Gly Phe Thr Ala Glu Asn Ile Val Ala
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Lys Ala His Lys Val Leu Gly Val Lys Gly Ala
 660 665

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<213> Artificial

<220>

<223> Primer JWF 430

<400> 13

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27

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<211> 29

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tagctctccg tcacgttact agatctcag

29

<210> 15

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<212> DNA

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<223> Primer JWF 484

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<210> 16

<211> 30

<212> DNA

<213> Artificial

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<223> Primer JWF 529

<400> 16

tagctctccg tcacgttact gacgtcgaag

30

<210> 17

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 501

<400> 17

gacaggaata aggagcatcg

20

<210> 18
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<220>
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<400> 18
ggagggtaaac ggtacgtggt

20

<210> 19
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 541

<400> 19
ggaattcgca taaacaggat cgccatca

28

<210> 20
<211> 26
<212> DNA
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<220>
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<400> 20
ctggatcctt aagccacgcg agccgt

26

<210> 21
<211> 29
<212> DNA
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<220>
<223> Primer JWF 610

<400> 21
gtggatcctt aatccgttca tagtgtaaa

29

<210> 22
<211> 27
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<220>
<223> Primer JWF 611

<400> 22
tgggatccat gagaaagccg actgcaa

27

<210> 23
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<212> DNA
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<220>
<223> Primer JWF 625

<400> 23
gttcgtcagt gcaggatgga

20

<210> 24
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 626

<400> 24
gttcaggcgt gagttttctg ct

22

<210> 25
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Primer JWF 541

<400> 25
ggaattcgca taaacaggat cgccatca

28

<210> 26
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<212> DNA
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<220>
<223> Primer JWF 542

<400> 26
ctggatcctt aagccacgag agccgt

26

<210> 27
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<212> DNA
<213> Artificial

<220>

<223> Primer JWF 636

<400> 27

tccgtactgc gcgtattgag a

21

<210> 28

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Primer JWF 637

<400> 28

agaggcgagt ttttcgacca

20

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<223> Primer JWF 669

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<212> DNA

<213> Artificial

<220>

<223> Primer JWF 599

<400> 31

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<210> 32

<211> 29
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<210> 33
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<210> 34
<211> 30
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<220>
<223> Primer JWF 529

<400> 34
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